

SEQUENCE LISTING

96 AUG -9 AM 4:49

(1) GENERAL INFORMATION:

(i) APPLICANT: Friedman, Jeffrey M.
Lee, Gwo-Hua
Proenca, Ricardo

(ii) TITLE OF INVENTION: DB, THE RECEPTOR FOR LEPTIN, NUCLEIC
ACIDS ENCODING THE RECEPTOR, AND USES THEREOF

(iii) NUMBER OF SEQUENCES: 54

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: David A. Jackson, Esq.
(B) STREET: 411 Hackensack Ave, Continental Plaza, 4th
Floor
(C) CITY: Hackensack
(D) STATE: New Jersey
(E) COUNTRY: USA
(F) ZIP: 07601

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/599,974
(B) FILING DATE: 14-FEB-1996
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/586,594
(B) FILING DATE: 16-JAN-1996
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Jackson Esq., David A.
(B) REGISTRATION NUMBER: 26,742
(C) REFERENCE/DOCKET NUMBER: 600-1-162 CP1

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 201-487-5800
(B) TELEFAX: 201-343-1684

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2821 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
CODING REGION: 1-2682

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: A15 (OB-Ra)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGATGTGTC	AGAAATTCTA	TGTGGTTTTG	TTACACTGGG	AATTTCTTTA	TGTGATAGCT	60
GCACTTAACC	TGGCATATCC	AATCTCTCCC	TGGAAATTTA	AGTTGTTTTG	TGGACCACCG	120
AACACAACCG	ATGACTCCTT	TCTCTCACCT	GCTGGAGCCC	CAAACAATGC	CTCGGCTTTG	180
AAGGGGGCTT	CTGAAGCAAT	TGTTGAAGCT	AAATTTAATT	CAAGTGGTAT	CTACGTTCCCT	240
GAGTTATCCA	AAACAGTCTT	CCACTGTTGC	TTTGGGAATG	AGCAAGGTCA	AAACTGCTCT	300
GCACTCACAG	ACAACACTGA	AGGGAAGACA	CTGGCTTCAG	TAGTGAAGGC	TTCAGTTTTT	360
CGCCAGCTAG	GTGTAAACTG	GGACATAGAG	TGCTGGATGA	AAGGGGACTT	GACATTATTC	420
ATCTGTCATA	TGGAGCCATT	ACCTAAGAAC	CCCTTCAAGA	ATTATGACTC	TAAGGTCCAT	480
CTTTTATATG	ATCTGCCTGA	AGTCATAGAT	GATTTCGCCTC	TGCCCCCACT	GAAAGACAGC	540
TTTCAGACTG	TCCAATGCAA	CTGCAGTCTT	CGGGGATGTG	AATGTCATGT	GCCGGTACCC	600
AGAGCCAAAC	TCAACTACGC	TCTTCTGATG	TATTTGGAAA	TCACATCTGC	CGGTGTGAGT	660
TTTCAGTCAC	CTCTGATGTC	ACTGCAGCCC	ATGCTTGTTG	TGAAACCCGA	TCCACCCTTA	720
GGTTTGCATA	TGGAAGTCAC	AGATGATGGT	AATTTAAAGA	TTTCTTGGA	CAGCCAAACA	780
ATGGCACCAT	TTCCGCTTCA	ATATCAGGTG	AAATATTTAG	AGAATTCTAC	AATTGTAAGA	840
GAGGCTGCTG	AAATTGTCTC	AGCTACATCT	CTGCTGGTAG	ACAGTGTGCT	TCCTGGATCT	900
TCATATGAGG	TCCAGGTGAG	GAGCAAGAGA	CTGGATGGTT	CAGGAGTCTG	GAGTGACTGG	960
AGTTCACCTC	AAGTCTTTAC	CACACAAGAT	GTTGTGTATT	TTCCACCCAA	AATTCTGACT	1020
AGTGTTGGAT	CGAATGCTTC	TTTTCATTCG	ATCTACAAAA	ACGAAAACCA	GATTATCTCC	1080
TCAAAACAGA	TAGTTTGGTG	GAGGAATCTA	GCTGAGAAAA	TCCCTGAGAT	ACAGTACAGC	1140
ATTGTGAGTG	ACCGAGTTAG	CAAAGTTACC	TTCTCCAACC	TGAAAGCCAC	CAGACCTCGA	1200
GGGAAGTTTA	CCTATGACGC	AGTGTACTGC	TGCAATGAGC	AGGCGTGCCA	TCACCGCTAT	1260

GCTGAATTAT	ACGTGATCGA	TGTCAATATC	AATATATCAT	GTGAAACTGA	CGGGTACTTA	1320
ACTAAAATGA	CTTGCAGATG	GTCACCCAGC	ACAATCCAAT	CACTAGTGGG	AAGCACTGTG	1380
CAGCTGAGGT	ATCACAGGCG	CAGCCTGTAT	TGTCCTGATA	GTCCATCTAT	TCATCCTACG	1440
TCTGAGCCCA	AAAACGTGCGT	CTTACAGAGA	GACGGCTTTT	ATGAATGTGT	TTTCCAGCCA	1500
ATCTTTCTAT	TATCTGGCTA	TACAATGTGG	ATCAGGATCA	ACCATTCTTT	AGGTTCACCT	1560
GACTCGCCAC	CAACGTGTGT	CCTTCCTGAC	TCCGTAGTAA	AACCACTACC	TCCATCTAAC	1620
GTAAAAGCAG	AGATTACTGT	AAACACTGGA	TTATTGAAAG	TATCTTGGGA	AAAGCCAGTC	1680
TTTCCGGAGA	ATAACCTTCA	ATTCCAGATT	CGATATGGCT	TAAGTGGAAG	AGAAATACAA	1740
TGGAAGACAC	ATGAGGTATT	CGATGCAAAG	TCAAAGTCTG	CCAGCCTGCT	GGTGTGAGAC	1800
CTCTGTGCAG	TCTATGTGGT	CCAGGTTTCG	TGCCGGCGGT	TGGATGGACT	AGGATATTGG	1860
AGTAATTGGA	GCAGTCCAGC	CTATACGCTT	GTCATGGATG	TAAAAGTTCC	TATGAGAGGG	1920
CCTGAATTTT	GGAGAAAAAT	GGATGGGGAC	GTTACTAAAA	AGGAGAGAAA	TGTCACCTTG	1980
CTTTGGAAGC	CCCTGACGAA	AAATGACTCA	CTGTGTAGTG	TGAGGAGGTA	CGTGGTGAAG	2040
CATCGTACTG	CCCACAATGG	GACGTGGTCA	GAAGATGTGG	GAAATCGGAC	CAATCTCACT	2100
TTCTGTGGA	CAGAACCAGC	GCACACTGTT	ACAGTTCTGG	CTGTCAATTC	CCTCGGCGCT	2160
TCCCTTGTGA	ATTTTAACCT	TACCTTCTCA	TGGCCCATGA	GTAAAGTGAG	TGCTGTGGAG	2220
TCCTCAGTG	CTTATCCCCT	GAGCAGCAGC	TGTGTCATCC	TTTCCTGGAC	ACTGTCACCT	2280
GATGATTATA	GTCTGTTATA	TCTGGTTATT	GAATGGAAGA	TCCTTAATGA	AGATGATGGA	2340
ATGAAGTGGC	TTAGAATTCC	CTCGAATGTT	AAAAAGTTTT	ATATCCACGA	TAATTTTATT	2400
CCCATCGAGA	AATATCAGTT	TAGTCTTTAC	CCAGTATTTA	TGGAAGGAGT	TGGAAAACCA	2460
AAGATAATTA	ATGGTTTCAC	CAAAGATGCT	ATCGACAAGC	AGCAGAATGA	CGCAGGGCTG	2520
TATGTCATTG	TACCCATAAT	TATTTCTCT	TGTGTCCTAC	TGCTCGGAAC	ACTGTTAATT	2580
TCACACCAGA	GAATGAAAAA	GTTGTTTTGG	GACGATGTTC	CAAACCCCAA	GAATTGTTCC	2640
TGGGCACAAG	GACTGAATTT	CCAAAAGAGA	ACGGACACTC	TTTGAAGTCT	CTCATGACCA	2700
CTACAGATGA	ACCCAATCTA	CCAACTTCCC	AACAGTCCAT	ACAATATTAG	AAGATGTTTA	2760
CATTTGGATG	GAGGGAAACA	ACCCTAAACT	ATGGTTTGAA	TGACTAAGAA	ATAACATTTG	2820
A						2821

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 894 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: OB-Ra

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Met	Cys	Gln	Lys	Phe	Tyr	Val	Val	Leu	Leu	His	Trp	Glu	Phe	Leu	1	5	10	15
Tyr	Val	Ile	Ala	Ala	Leu	Asn	Leu	Ala	Tyr	Pro	Ile	Ser	Pro	Trp	Lys	20	25	30	
Phe	Lys	Leu	Phe	Cys	Gly	Pro	Pro	Asn	Thr	Thr	Asp	Asp	Ser	Phe	Leu	35	40	45	
Ser	Pro	Ala	Gly	Ala	Pro	Asn	Asn	Ala	Ser	Ala	Leu	Lys	Gly	Ala	Ser	50	55	60	
Glu	Ala	Ile	Val	Glu	Ala	Lys	Phe	Asn	Ser	Ser	Gly	Ile	Tyr	Val	Pro	65	70	75	80
Glu	Leu	Ser	Lys	Thr	Val	Phe	His	Cys	Cys	Phe	Gly	Asn	Glu	Gln	Gly	85	90	95	
Gln	Asn	Cys	Ser	Ala	Leu	Thr	Asp	Asn	Thr	Glu	Gly	Lys	Thr	Leu	Ala	100	105	110	
Ser	Val	Val	Lys	Ala	Ser	Val	Phe	Arg	Gln	Leu	Gly	Val	Asn	Trp	Asp	115	120	125	
Ile	Glu	Cys	Trp	Met	Lys	Gly	Asp	Leu	Thr	Leu	Phe	Ile	Cys	His	Met	130	135	140	
Glu	Pro	Leu	Pro	Lys	Asn	Pro	Phe	Lys	Asn	Tyr	Asp	Ser	Lys	Val	His	145	150	155	160
Leu	Leu	Tyr	Asp	Leu	Pro	Glu	Val	Ile	Asp	Asp	Ser	Pro	Leu	Pro	Pro	165	170	175	
Leu	Lys	Asp	Ser	Phe	Gln	Thr	Val	Gln	Cys	Asn	Cys	Ser	Leu	Arg	Gly	180	185	190	
Cys	Glu	Cys	His	Val	Pro	Val	Pro	Arg	Ala	Lys	Leu	Asn	Tyr	Ala	Leu				

195					200					205					
Leu	Met	Tyr	Leu	Glu	Ile	Thr	Ser	Ala	Gly	Val	Ser	Phe	Gln	Ser	Pro
210						215					220				
Leu	Met	Ser	Leu	Gln	Pro	Met	Leu	Val	Val	Lys	Pro	Asp	Pro	Pro	Leu
225					230					235					240
Gly	Leu	His	Met	Glu	Val	Thr	Asp	Asp	Gly	Asn	Leu	Lys	Ile	Ser	Trp
				245					250					255	
Asp	Ser	Gln	Thr	Met	Ala	Pro	Phe	Pro	Leu	Gln	Tyr	Gln	Val	Lys	Tyr
			260					265					270		
Leu	Glu	Asn	Ser	Thr	Ile	Val	Arg	Glu	Ala	Ala	Glu	Ile	Val	Ser	Ala
		275					280					285			
Thr	Ser	Leu	Leu	Val	Asp	Ser	Val	Leu	Pro	Gly	Ser	Ser	Tyr	Glu	Val
	290					295					300				
Gln	Val	Arg	Ser	Lys	Arg	Leu	Asp	Gly	Ser	Gly	Val	Trp	Ser	Asp	Trp
305					310					315					320
Ser	Ser	Pro	Gln	Val	Phe	Thr	Thr	Gln	Asp	Val	Val	Tyr	Phe	Pro	Pro
				325					330					335	
Lys	Ile	Leu	Thr	Ser	Val	Gly	Ser	Asn	Ala	Ser	Phe	His	Cys	Ile	Tyr
			340					345					350		
Lys	Asn	Glu	Asn	Gln	Ile	Ile	Ser	Ser	Lys	Gln	Ile	Val	Trp	Trp	Arg
	355						360					365			
Asn	Leu	Ala	Glu	Lys	Ile	Pro	Glu	Ile	Gln	Tyr	Ser	Ile	Val	Ser	Asp
	370					375					380				
Arg	Val	Ser	Lys	Val	Thr	Phe	Ser	Asn	Leu	Lys	Ala	Thr	Arg	Pro	Arg
385					390					395					400
Gly	Lys	Phe	Thr	Tyr	Asp	Ala	Val	Tyr	Cys	Cys	Asn	Glu	Gln	Ala	Cys
				405					410					415	
His	His	Arg	Tyr	Ala	Glu	Leu	Tyr	Val	Ile	Asp	Val	Asn	Ile	Asn	Ile
			420					425					430		
Ser	Cys	Glu	Thr	Asp	Gly	Tyr	Leu	Thr	Lys	Met	Thr	Cys	Arg	Trp	Ser
		435					440					445			
Pro	Ser	Thr	Ile	Gln	Ser	Leu	Val	Gly	Ser	Thr	Val	Gln	Leu	Arg	Tyr
	450					455					460				
His	Arg	Arg	Ser	Leu	Tyr	Cys	Pro	Asp	Ser	Pro	Ser	Ile	His	Pro	Thr
465					470					475					480
Ser	Glu	Pro	Lys	Asn	Cys	Val	Leu	Gln	Arg	Asp	Gly	Phe	Tyr	Glu	Cys
				485					490					495	
Val	Phe	Gln	Pro	Ile	Phe	Leu	Leu	Ser	Gly	Tyr	Thr	Met	Trp	Ile	Arg
			500					505					510		

Ile	Asn	His	Ser	Leu	Gly	Ser	Leu	Asp	Ser	Pro	Pro	Thr	Cys	Val	Leu
		515					520					525			
Pro	Asp	Ser	Val	Val	Lys	Pro	Leu	Pro	Pro	Ser	Asn	Val	Lys	Ala	Glu
	530					535					540				
Ile	Thr	Val	Asn	Thr	Gly	Leu	Leu	Lys	Val	Ser	Trp	Glu	Lys	Pro	Val
545					550					555					560
Phe	Pro	Glu	Asn	Asn	Leu	Gln	Phe	Gln	Ile	Arg	Tyr	Gly	Leu	Ser	Gly
				565					570					575	
Lys	Glu	Ile	Gln	Trp	Lys	Thr	His	Glu	Val	Phe	Asp	Ala	Lys	Ser	Lys
			580					585					590		
Ser	Ala	Ser	Leu	Leu	Val	Ser	Asp	Leu	Cys	Ala	Val	Tyr	Val	Val	Gln
		595					600					605			
Val	Arg	Cys	Arg	Arg	Leu	Asp	Gly	Leu	Gly	Tyr	Trp	Ser	Asn	Trp	Ser
	610					615					620				
Ser	Pro	Ala	Tyr	Thr	Leu	Val	Met	Asp	Val	Lys	Val	Pro	Met	Arg	Gly
625					630					635					640
Pro	Glu	Phe	Trp	Arg	Lys	Met	Asp	Gly	Asp	Val	Thr	Lys	Lys	Glu	Arg
				645					650					655	
Asn	Val	Thr	Leu	Leu	Trp	Lys	Pro	Leu	Thr	Lys	Asn	Asp	Ser	Leu	Cys
			660					665					670		
Ser	Val	Arg	Arg	Tyr	Val	Val	Lys	His	Arg	Thr	Ala	His	Asn	Gly	Thr
		675					680					685			
Trp	Ser	Glu	Asp	Val	Gly	Asn	Arg	Thr	Asn	Leu	Thr	Phe	Leu	Trp	Thr
	690					695					700				
Glu	Pro	Ala	His	Thr	Val	Thr	Val	Leu	Ala	Val	Asn	Ser	Leu	Gly	Ala
705					710					715					720
Ser	Leu	Val	Asn	Phe	Asn	Leu	Thr	Phe	Ser	Trp	Pro	Met	Ser	Lys	Val
				725					730					735	
Ser	Ala	Val	Glu	Ser	Leu	Ser	Ala	Tyr	Pro	Leu	Ser	Ser	Ser	Cys	Val
			740					745					750		
Ile	Leu	Ser	Trp	Thr	Leu	Ser	Pro	Asp	Asp	Tyr	Ser	Leu	Leu	Tyr	Leu
		755					760					765			
Val	Ile	Glu	Trp	Lys	Ile	Leu	Asn	Glu	Asp	Asp	Gly	Met	Lys	Trp	Leu
						775					780				
Arg	Ile	Pro	Ser	Asn	Val	Lys	Lys	Phe	Tyr	Ile	His	Asp	Asn	Phe	Ile
785					790					795					800
Pro	Ile	Glu	Lys	Tyr	Gln	Phe	Ser	Leu	Tyr	Pro	Val	Phe	Met	Glu	Gly
				805					810					815	

Val	Gly	Lys	Pro	Lys	Ile	Ile	Asn	Gly	Phe	Thr	Lys	Asp	Ala	Ile	Asp	
			820					825					830			
Lys	Gln	Gln	Asn	Asp	Ala	Gly	Leu	Tyr	Val	Ile	Val	Pro	Ile	Ile	Ile	
		835					840					845				
Ser	Ser	Cys	Val	Leu	Leu	Leu	Gly	Thr	Leu	Leu	Ile	Ser	His	Gln	Arg	
	850					855					860					
Met	Lys	Lys	Leu	Phe	Trp	Asp	Asp	Val	Pro	Asn	Pro	Lys	Asn	Cys	Ser	
865					870					875					880	
Trp	Ala	Gln	Gly	Leu	Asn	Phe	Gln	Lys	Arg	Thr	Asp	Thr	Leu			
				885					890							

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2914 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
CODING REGION: 1349-2845
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: A40 (OB-Rb)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTCATTGAGA GTGCCAACGG GAAGGCTTAA TTAACCTTTG GAANTGAGTC CGAAGAGTCT	60
GGAAGTNTGT AAGATGGAAG ATACTATACA AGATACTTCA GAGCTGTACA TTCTTCCAGG	120
GATGTAGGCT AGCAGTTATT TCATTAGTAT ATGTCTATTT TAGAATGGGA AGAATTAGGA	180
AGATGAATGG AGCCTGTGTC TTTCACTACT CTCCCAGGAG GTTCCAGAAT AGCNAAAGTG	240
TCAGCCAGAA TTCTTGAAGT CATAGACTGG AGTTAGAGAT GAACATAAGC TCATGTTAAG	300
CCTGGGTTAC TTCTTATCAT CCTTAATTTT GAAAGCTAAG AGGGCCTAAC CATCAAGAAC	360
GTCCTGGAGG AAAGAATGTT TTTAACGCCA TTATTTCAGTC AAAGAAATTA AGACTTGAGA	420
GAAATGCTCA TTTCTTCTCT CATGATGGCT CCTTACACCT TACTTCTACC GTACGATCCA	480
TGNGGCCCTA CCCACGCAGG ATACATGCAT CTATATGAGA GTGTCTNCCC CTTCTAACTC	540

AGAGACTCTT	GTTCTAGTCT	GTGNTATAAA	ATTCAGCTTG	TGGAAGCTTT	CTGAGGGGTT	600
GGCAGCATT	AATTTTACCT	GCAATAGGTA	AAGGTAATCT	TTTGGGAAGT	GAAGAGTGTT	660
ATTAGACATT	TCAGAAAGAA	CAAACAGGAT	TGGGGCTGCT	ATGTGTTCTA	CACAGGAATC	720
TTCCATAACA	CAGAATAATT	TATGTAGATA	GAGACAAGAT	GGAAATGCCC	AGGGCCCCAA	780
AATAGCCGCT	GTTATTTGTT	AACCTTCAAG	GTTTTCTGTT	TGTTTATCTG	TTTCTTGCGC	840
AGGATCATCT	TCCAAGCACA	TCCTGGGGGA	ACAGTGGCAG	AGTCACTCGA	GTTCATGAAA	900
CTATGGTGAC	ATCTGAGCTT	CCTTGGTTCT	TCACAGAACA	TAAGCAGTTC	CTTTGCTTGC	960
TTGTTAGATG	AGAAAACCTC	CTTGTCAGTC	TGTCTCTACG	ACTAGAATGG	AAAGCCTTAC	1020
TACTTCCTAT	GTATTCTTAA	TATTTCAAAT	GTCCTAATTA	TGTTTGGCTT	CTCTGTCTTT	1080
AAGGGATTTA	GTCTCTGGAT	TTGAAGAAAT	AAATAAATAA	ATAAAGGAAA	ACTAATTTTC	1140
TCGTGCCGGA	TGACTGCTAG	CTGAGCTCAG	GCCTACTGCA	TTCTACATTT	CGACTCTCTC	1200
CCTCTTCCCC	AGTGCTTTAG	CACTGGACTG	GGCAGTNCCT	GGCCTGGTCT	AACTCCTGTT	1260
TCCTGGTG	GGG AATGTATAAT	AAGAACTCCA	TGAGTTCTGG	TATAAACACT	GTGGTCTGTG	1320
TGCTAATTAA	ATCTNGTGTT	TCCTACAGCC	CCTGACGAAA	AATGACTCAC	TGTGTAGTGT	1380
GAGGAGGTAC	GTGGTGAAGC	ATCGTACTGC	CCACAATGGG	ACGTGGTCAG	AAGATGTGGG	1440
AAATCGGACC	AATCTCACTT	TCCTGTGGAC	AGAACCAGCG	CACACTGTTA	CAGTTCTGGC	1500
TGTCAATTCC	CTCGGCGCTT	CCCTTGTGAA	TTTTAACCTT	ACCTTCTCAT	GGCCCATGAG	1560
TAAAGTGAGT	GCTGTGGAGT	CACTCAGTGC	TTATCCCCTG	AGCAGCAGCT	GTGTCATCCT	1620
TTCTTGACA	CTGTACCTG	ATGATTATAG	TCTGTTATAT	CTGGTTATTG	AATGGAAGAT	1680
CCTTAATGAA	GATGATGGAA	TGAAGTGGCT	TAGAATTCCC	TCGAATGTTA	AAAAGTTTTA	1740
TATCCACGAT	AATTTTATTC	CCATCGAGAA	ATATCAGTTT	AGTCTTTACC	CAGTATTTAT	1800
GGAAGGAGTT	GGAAAACCAA	AGATAATTAA	TGGTTTCACC	AAAGATGCTA	TCGACAAGCA	1860
GCAGAATGAC	GCAGGGCTGT	ATGTCATTGT	ACCCATAATT	ATTTCTCTCT	GTGTCCTACT	1920
GCTCGGAACA	CTGTTAATTT	CACACCAGAG	AATGAAAAAG	TTGTTTTGGG	ACGATGTTCC	1980
AAACCCCAAG	AATTGTTTCT	GGGCACAAGG	ACTGAATTTT	CAAAAGCCTG	AAACATTTGA	2040
GCATCTTTTT	ACCAAGCATG	CAGAATCAGT	GATATTTGGT	CCTCTTCTTC	TGGAGCCTGA	2100
ACCCATTTCA	GAAGAAATCA	GTGTCGATAC	AGCTTGAAAA	AATAAAGATG	AGATGGTCCC	2160
AGCAGCTATG	GTCTCCCTTC	TTTTGACCAC	ACCAGACCCT	GAAAGCAGTT	CTATTTGTAT	2220
TAGTGACCAG	TGTAACAGTG	CTAACTTCTC	TGGGTCTCAG	AGCACCCAGG	TAACCTGTGA	2280

GGATGAGTGT CAGAGACAAC CCTCAGTTAA ATATGCAACT CTGGTCAGCA ACGATAAACT	2340
AGTGGAAGT GATGAAGAGC AAGGGTTTAT CCATAGTCCT GTCAGCAACT GCATCTCCAG	2400
TAATCATTC CCACTGAGGC AGTCTTTCTC TAGCAGCTCC TGGGAGACAG AGGCCCAGAC	2460
ATTTTTCCTT TTATCAGACC AGCAACCCAC CATGATTTC CAACAACCTT CATTCTCGGG	2520
GTTGGATGAG CTTTTGGAAC TGGAGGGAAG TTTTCCTGAA GAAAATCACA GGGAGAAGTC	2580
TGTCTGTTAT CTAGGAGTCA CCTCCGTCAA CAGAAGAGAG AGTGGTGTGC TTTTGACTGG	2640
TGAGGCAGGA ATCCTGTGCA CATTCCCAGC CCAGTGTCTG TTCAGTGACA TCAGGATCCT	2700
CCAGGAGAGA TGCTCACACT TTGTAGAAAA TAATTTGAGT TTAGGGACCT CTGGTGAGAA	2760
CTTTGTACCT TACATGCCCC AATTTCAAAC CTGTTCCACG CACAGTCACA AGATAATGGA	2820
GAATAAGATG TGTGACTTAA CTGTGTAATC TCATCCAAGA AGCCTCAAGG TTCCATTCCA	2880
GTAGAGCCTG TCATGTATAA TGTGTTCTTT ATTG	2914

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 499 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: OB-Rb

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Pro	Leu	Thr	Lys	Asn	Asp	Ser	Leu	Cys	Ser	Val	Arg	Arg	Tyr	Val	Val
1				5					10					15	
Lys	His	Arg	Thr	Ala	His	Asn	Gly	Thr	Trp	Ser	Glu	Asp	Val	Gly	Asn
			20					25					30		
Arg	Thr	Asn	Leu	Thr	Phe	Leu	Trp	Thr	Glu	Pro	Ala	His	Thr	Val	Thr
		35					40					45			
Val	Leu	Ala	Val	Asn	Ser	Leu	Gly	Ala	Ser	Leu	Val	Asn	Phe	Asn	Leu
	50						55				60				

Thr	Phe	Ser	Trp	Pro	Met	Ser	Lys	Val	Ser	Ala	Val	Glu	Ser	Leu	Ser		
65					70					75					80		
Ala	Tyr	Pro	Leu	Ser	Ser	Ser	Cys	Val	Ile	Leu	Ser	Trp	Thr	Leu	Ser		
				85					90					95			
Pro	Asp	Asp	Tyr	Ser	Leu	Leu	Tyr	Leu	Val	Ile	Glu	Trp	Lys	Ile	Leu		
			100					105					110				
Asn	Glu	Asp	Asp	Gly	Met	Lys	Trp	Leu	Arg	Ile	Pro	Ser	Asn	Val	Lys		
		115					120						125				
Lys	Phe	Tyr	Ile	His	Asp	Asn	Phe	Ile	Pro	Ile	Glu	Lys	Tyr	Gln	Phe		
	130					135					140						
Ser	Leu	Tyr	Pro	Val	Phe	Met	Glu	Gly	Val	Gly	Lys	Pro	Lys	Ile	Ile		
145					150					155					160		
Asn	Gly	Phe	Thr	Lys	Asp	Ala	Ile	Asp	Lys	Gln	Gln	Asn	Asp	Ala	Gly		
				165					170					175			
Leu	Tyr	Val	Ile	Val	Pro	Ile	Ile	Ile	Ser	Ser	Cys	Val	Leu	Leu	Leu		
			180					185					190				
Gly	Thr	Leu	Leu	Ile	Ser	His	Gln	Arg	Met	Lys	Lys	Leu	Phe	Trp	Asp		
		195					200						205				
Asp	Val	Pro	Asn	Pro	Lys	Asn	Cys	Ser	Trp	Ala	Gln	Gly	Leu	Asn	Phe		
	210					215					220						
Gln	Lys	Pro	Glu	Thr	Phe	Glu	His	Leu	Phe	Thr	Lys	His	Ala	Glu	Ser		
225					230					235					240		
Val	Ile	Phe	Gly	Pro	Leu	Leu	Leu	Glu	Pro	Glu	Pro	Ile	Ser	Glu	Glu		
				245				250						255			
Ile	Ser	Val	Asp	Thr	Ala	Trp	Lys	Asn	Lys	Asp	Glu	Met	Val	Pro	Ala		
			260					265					270				
Ala	Met	Val	Ser	Leu	Leu	Leu	Thr	Thr	Pro	Asp	Pro	Glu	Ser	Ser	Ser		
		275					280					285					
Ile	Cys	Ile	Ser	Asp	Gln	Cys	Asn	Ser	Ala	Asn	Phe	Ser	Gly	Ser	Gln		
	290					295					300						
Ser	Thr	Gln	Val	Thr	Cys	Glu	Asp	Glu	Cys	Gln	Arg	Gln	Pro	Ser	Val		
305					310					315					320		
Lys	Tyr	Ala	Thr	Leu	Val	Ser	Asn	Asp	Lys	Leu	Val	Glu	Thr	Asp	Glu		
				325					330					335			
Glu	Gln	Gly	Phe	Ile	His	Ser	Pro	Val	Ser	Asn	Cys	Ile	Ser	Ser	Asn		
			340					345					350				
His	Ser	Pro	Leu	Arg	Gln	Ser	Phe	Ser	Ser	Ser	Ser	Trp	Glu	Thr	Glu		
		355					360					365					
Ala	Gln	Thr	Phe	Phe	Leu	Leu	Ser	Asp	Gln	Gln	Pro	Thr	Met	Ile	Ser		

370		375		380
Pro Gln Leu Ser Phe Ser Gly Leu Asp Glu Leu Leu Glu Leu Glu Gly				
385		390		395 400
Ser Phe Pro Glu Glu Asn His Arg Glu Lys Ser Val Cys Tyr Leu Gly				
	405		410	415
Val Thr Ser Val Asn Arg Arg Glu Ser Gly Val Leu Leu Thr Gly Glu				
	420		425	430
Ala Gly Ile Leu Cys Thr Phe Pro Ala Gln Cys Leu Phe Ser Asp Ile				
	435		440	445
Arg Ile Leu Gln Glu Arg Cys Ser His Phe Val Glu Asn Asn Leu Ser				
	450		455	460
Leu Gly Thr Ser Gly Glu Asn Phe Val Pro Tyr Met Pro Gln Phe Gln				
	465		470	475 480
Thr Cys Ser Thr His Ser His Lys Ile Met Glu Asn Lys Met Cys Asp				
	485		490	495
Leu Thr Val				

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1240 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
 - CODING REGION: 272-958
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: A6 (OB-Rc)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TTTAAGGGAT TTAGTCTCTG GATTTGAAGA AATAAATAAA TAAATAAAGG AAAACTAATT	60
TTCTCGTGCC GGATGACTGC TAGCTGAGCT CAGGCCTACT GCATTCTACA TTTCGACTCT	120
CTCCCTCTTC CCCAGTGCTT TAGCACTGGA CTGGGCAGTN CCTGGCCTGG TCTAACTCCT	180
GTTTCCTGGT GGGAATGTAT AATAAGAACT CCATGAGTTC TGGTATAAAC ACTGTGGTCT	240

GTGTGCTAAT TAAATCTNGT GTTTCCTACA GCCCCTGACG AAAAATGACT CACTGTGTAG	300
TGTGAGGAGG TACGTGGTGA AGCATCGTAC TGCCCACAAT GGGACGTGGT CAGAAGATGT	360
GGGAAATCGG ACCAATCTCA CTTTCCTGTG GACAGAACCA GCGCACACTG TTACAGTTCT	420
GGCTGTCAAT TCCCTCGGCG CTTCCCTTGT GAATTTTAAC CTTACCTTCT CATGGCCCAT	480
GAGTAAAGTG AGTGCTGTGG AGTCACTCAG TGCTTATCCC CTGAGCAGCA GCTGTGTCAT	540
CCTTTCCTGG ACACTGTCAC CTGATGATTA TAGTCTGTTA TATCTGGTTA TTGAATGGAA	600
GATCCTTAAT GAAGATGATG GAATGAAGTG GCTTAGAATT CCCTCGAATG TTAAAAAGTT	660
TTATATCCAC GATAATTTTA TTCCCATCGA GAAATATCAG TTTAGTCTTT ACCCAGTATT	720
TATGGAAGGA GTTGGAAGAAC CAAAGATAAT TAATGGTTTC ACCAAAGATG CTATCGACAA	780
GCAGCAGAAT GACGCAGGGC TGTATGTCAT TGTACCCATA ATTATTTCCCT CTTGTGTCCT	840
ACTGCTCGGA ACACTGTTAA TTTCACACCA GAGAATGAAA AAGTTGTTTT GGGACGATGT	900
TCCAAACCCC AAGAATTGTT CCTGGGCACA AGGACTGAAT TTCCAAAAGG TCACTGTTTA	960
AGTATTTTAA CCCAGATATC TAAGGTTGCA GTTTAGATGC CACAGTACTT ACAGATCTTT	1020
AAACAACCTT AAAGGGCTTT ATGTTGTTGT GTTCATGTTT TCAAGCCTGT TCATCCTTTC	1080
TCTTTCTCAA AAGCTGGGTT TGGGATTTGA TCAGAGAAAA CAAAGTTCGC TCCCTTATCT	1140
CATGAGAGTT GACAACACAT CTATCTCTCT TTCTGCTTAC TGTACATAAA AAAAATAAAT	1200
ACTACAAGAG GAAGGAATGT TATAGATGGA GAATAGATAG	1240

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 229 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: OB-Rc
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Pro	Leu	Thr	Lys	Asn	Asp	Ser	Leu	Cys	Ser	Val	Arg	Arg	Tyr	Val	Val	1	5	10	15
Lys	His	Arg	Thr	Ala	His	Asn	Gly	Thr	Trp	Ser	Glu	Asp	Val	Gly	Asn	20	25	30	
Arg	Thr	Asn	Leu	Thr	Phe	Leu	Trp	Thr	Glu	Pro	Ala	His	Thr	Val	Thr	35	40	45	
Val	Leu	Ala	Val	Asn	Ser	Leu	Gly	Ala	Ser	Leu	Val	Asn	Phe	Asn	Leu	50	55	60	
Thr	Phe	Ser	Trp	Pro	Met	Ser	Lys	Val	Ser	Ala	Val	Glu	Ser	Leu	Ser	65	70	75	
Ala	Tyr	Pro	Leu	Ser	Ser	Ser	Cys	Val	Ile	Leu	Ser	Trp	Thr	Leu	Ser	85	90	95	
Pro	Asp	Asp	Tyr	Ser	Leu	Leu	Tyr	Leu	Val	Ile	Glu	Trp	Lys	Ile	Leu	100	105	110	
Asn	Glu	Asp	Asp	Gly	Met	Lys	Trp	Leu	Arg	Ile	Pro	Ser	Asn	Val	Lys	115	120	125	
Lys	Phe	Tyr	Ile	His	Asp	Asn	Phe	Ile	Pro	Ile	Glu	Lys	Tyr	Gln	Phe	130	135	140	
Ser	Leu	Tyr	Pro	Val	Phe	Met	Glu	Gly	Val	Gly	Lys	Pro	Lys	Ile	Ile	145	150	155	
Asn	Gly	Phe	Thr	Lys	Asp	Ala	Ile	Asp	Lys	Gln	Gln	Asn	Asp	Ala	Gly	165	170	175	
Leu	Tyr	Val	Ile	Val	Pro	Ile	Ile	Ile	Ser	Ser	Cys	Val	Leu	Leu	Leu	180	185	190	
Gly	Thr	Leu	Leu	Ile	Ser	His	Gln	Arg	Met	Lys	Lys	Leu	Phe	Trp	Asp	195	200	205	
Asp	Val	Pro	Asn	Pro	Lys	Asn	Cys	Ser	Trp	Ala	Gln	Gly	Leu	Asn	Phe	210	215	220	
Gln	Lys	Val	Thr	Val	225														

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2892 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

CODING REGION: 1-2700

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: A8 (OB-Rd)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATGATGTGTC	AGAAATTCTA	TGTGGTTTTG	TTACACTGGG	AATTTCTTTA	TGTGATAGCT	60
GCACTTAACC	TGGCATATCC	AATCTCTCCC	TGGAAATTTA	AGTTGTTTTG	TGGACCACCG	120
AACACAACCG	ATGACTCCTT	TCTCTCACCT	GCTGGAGCCC	CAAACAATGC	CTCGGCTTTG	180
AAGGGGGCTT	CTGAAGCAAT	TGTTGAAGCT	AAATTTAATT	CAAGTGGTAT	CTACGTTCCCT	240
GAGTTATCCA	AAACAGTCTT	CCACTGTTGC	TTTGGGAATG	AGCAAGGTCA	AAACTGCTCT	300
GCACTCACAG	ACAACACTGA	AGGGAAGACA	CTGGCTTCAG	TAGTGAAGGC	TTCAGTTTTT	360
CGCCAGCTAG	GTGTAAACTG	GGACATAGAG	TGCTGGATGA	AAGGGGACTT	GACATTATTC	420
ATCTGTCATA	TGGAGCCATT	ACCTAAGAAC	CCCTTCAAGA	ATTATGACTC	TAAGGTCCAT	480
CTTTTATATG	ATCTGCCTGA	AGTCATAGAT	GATTGCCTC	TGCCCCCACT	GAAAGACAGC	540
TTTCAGACTG	TCCAATGCAA	CTGCAGTCTT	CGGGGATGTG	AATGTCATGT	GCCGGTACCC	600
AGAGCCAAAC	TCAACTACGC	TCTTCTGATG	TATTTGGAAA	TCACATCTGC	CGGTGTGAGT	660
TTTCAGTCAC	CTCTGATGTC	ACTGCAGCCC	ATGCTTGTTG	TGAAACCCGA	TCCACCCTTA	720
GGTTTGCATA	TGGAAGTCAC	AGATGATGGT	AATTTAAAGA	TTTCTTGGA	CAGCCAAACA	780
ATGGCACCAT	TTCCGCTTCA	ATATCAGGTG	AAATATTTAG	AGAATTCTAC	AATTGTAAGA	840
GAGGCTGCTG	AAATTGTCTC	AGCTACATCT	CTGCTGGTAG	ACAGTGTGCT	TCCTGGATCT	900
TCATATGAGG	TCCAGGTGAG	GAGCAAGAGA	CTGGATGGTT	CAGGAGTCTG	GAGTGACTGG	960
AGTTCACCTC	AAGTCTTTAC	CACACAAGAT	GTTGTGTATT	TTCCACCCAA	AATTCTGACT	1020
AGTGTTGGAT	CGAATGCTTC	TTTTCATTGC	ATCTACAAAA	ACGAAAACCA	GATTATCTCC	1080
TCAAAACAGA	TAGTTTGGTG	GAGGAATCTA	GCTGAGAAAA	TCCCTGAGAT	ACAGTACAGC	1140
ATTGTGAGTG	ACCGAGTTAG	CAAAGTTACC	TTCTCCAACC	TGAAAGCCAC	CAGACCTCGA	1200
GGGAAGTTTA	CCTATGACGC	AGTGTACTGC	TGCAATGAGC	AGGCGTGCCA	TCACCGCTAT	1260
GCTGAATTAT	ACGTGATCGA	TGTCAATATC	AATATATCAT	GTGAAACTGA	CGGGTACTTA	1320
ACTAAAATGA	CTTGCAGATG	GTCACCCAGC	ACAATCCAAT	CACTAGTGGG	AAGCACTGTG	1380

CAGCTGAGGT ATCACAGGCG CAGCCTGTAT TGTCCTGATA GTCCATCTAT TCATCCTACG	1440
TCTGAGCCCA AAAACTGCGT CTTACAGAGA GACGGCTTTT ATGAATGTGT TTTCCAGCCA	1500
ATCTTTCTAT TATCTGGCTA TACAATGTGG ATCAGGATCA ACCATTCTTT AGGTTCACCT	1560
GACTCGCCAC CAACGTGTGT CCTTCCTGAC TCCGTAGTAA AACCCTACC TCCATCTAAC	1620
GTAAAAGCAG AGATTACTGT AAACACTGGA TTATTGAAAG TATCTTGGA AAAGCCAGTC	1680
TTTCCGGAGA ATAACCTTCA ATTCCAGATT CGATATGGCT TAAGTGGAAG AGAAATACAA	1740
TGGAAGACAC ATGAGGTATT CGATGCAAAG TCAAAGTCTG CCAGCCTGCT GGTGTCAGAC	1800
CTCTGTGCAG TCTATGTGGT CCAGGTTTCG TGCCGGCGGT TGGATGGACT AGGATATTGG	1860
AGTAATTGGA GCAGTCCAGC CTATACGCTT GTCATGGATG TAAAAGTTCC TATGAGAGGG	1920
CCTGAATTTT GGAGAAAAAT GGATGGGGAC GTTACTAAAA AGGAGAGAAA TGTCACCTTG	1980
CTTTGGAAGC CCCTGACGAA AAATGACTCA CTGTGTAGTG TGAGGAGGTA CGTGGTGAAG	2040
CATCGTACTG CCCACAATGG GACGTGGTCA GAAGATGTGG GAAATCGGAC CAATCTCACT	2100
TTCCTGTGGA CAGAACCAGC GCACACTGTT ACAGTTCTGG CTGTCAATTC CCTCGGCGCT	2160
TCCCTTGTGA ATTTTAACCT TACCTTCTCA TGGCCCATGA GTAAAGTGAG TGCTGTGGAG	2220
TCCTCAGTG CTTATCCCCT GAGCAGCAGC TGTGTCATCC TTTCTGGAC ACTGTCACCT	2280
GATGATTATA GTCTGTTATA TCTGGTTATT GAATGGAAGA TCCTTAATGA AGATGATGGA	2340
ATGAAGTGGC TTAGAATTCC CTCGAATGTT AAAAAGTTTT ATATCCACGA TAATTTTATT	2400
CCCATCGAGA AATATCAGTT TAGTCTTTAC CCAGTATTTA TGGAAGGAGT TGGAAAACCA	2460
AAGATAATTA ATGGTTTCAC CAAAGATGCT ATCGACAAGC AGCAGAATGA CGCAGGGCTG	2520
TATGTCATTG TACCCATAAT TATTTCTCT TGTGTCCTAC TGCTCGGAAC ACTGTTAATT	2580
TCACACCAGA GAATGAAAAA GTTGTTTTGG GACGATGTTT CAAACCCCAA GAATTGTTCC	2640
TGGGCACAAG GACTGAATTT CCAAAGGAT ATATCTTTAC ATGAAGTTTT TATTTTCAGA	2700
TAGCCTCTGG CAGATTCTCA CTGTGGCCTG AGGCAGCCTG AAACATTTGA GCATCTTTTT	2760
ACCAAGCATG CAGAATCAGT GATATTTGGT CCTCTTCTTC TGGAGCCTGA ACCCATTTCA	2820
GAAGAAATCA GTGTCGATAC AGCTTGGAAG AATAAAGATG AGATGGTCCC AGCAGCTATG	2880
GTCTCCCTTC TT	2892

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 900 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: OB-Rd

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Met	Cys	Gln	Lys	Phe	Tyr	Val	Val	Leu	Leu	His	Trp	Glu	Phe	Leu	
1				5					10					15		
Tyr	Val	Ile	Ala	Ala	Leu	Asn	Leu	Ala	Tyr	Pro	Ile	Ser	Pro	Trp	Lys	
			20					25					30			
Phe	Lys	Leu	Phe	Cys	Gly	Pro	Pro	Asn	Thr	Thr	Asp	Asp	Ser	Phe	Leu	
		35						40				45				
Ser	Pro	Ala	Gly	Ala	Pro	Asn	Asn	Ala	Ser	Ala	Leu	Lys	Gly	Ala	Ser	
	50					55					60					
Glu	Ala	Ile	Val	Glu	Ala	Lys	Phe	Asn	Ser	Ser	Gly	Ile	Tyr	Val	Pro	
65					70					75					80	
Glu	Leu	Ser	Lys	Thr	Val	Phe	His	Cys	Cys	Phe	Gly	Asn	Glu	Gln	Gly	
				85					90					95		
Gln	Asn	Cys	Ser	Ala	Leu	Thr	Asp	Asn	Thr	Glu	Gly	Lys	Thr	Leu	Ala	
			100					105					110			
Ser	Val	Val	Lys	Ala	Ser	Val	Phe	Arg	Gln	Leu	Gly	Val	Asn	Trp	Asp	
		115					120					125				
Ile	Glu	Cys	Trp	Met	Lys	Gly	Asp	Leu	Thr	Leu	Phe	Ile	Cys	His	Met	
	130					135					140					
Glu	Pro	Leu	Pro	Lys	Asn	Pro	Phe	Lys	Asn	Tyr	Asp	Ser	Lys	Val	His	
145					150					155					160	
Leu	Leu	Tyr	Asp	Leu	Pro	Glu	Val	Ile	Asp	Asp	Ser	Pro	Leu	Pro	Pro	
				165					170					175		
Leu	Lys	Asp	Ser	Phe	Gln	Thr	Val	Gln	Cys	Asn	Cys	Ser	Leu	Arg	Gly	
			180					185					190			
Cys	Glu	Cys	His	Val	Pro	Val	Pro	Arg	Ala	Lys	Leu	Asn	Tyr	Ala	Leu	
		195					200					205				

Leu	Met	Tyr	Leu	Glu	Ile	Thr	Ser	Ala	Gly	Val	Ser	Phe	Gln	Ser	Pro	210	215	220	
Leu	Met	Ser	Leu	Gln	Pro	Met	Leu	Val	Val	Lys	Pro	Asp	Pro	Pro	Leu	225	230	235	240
Gly	Leu	His	Met	Glu	Val	Thr	Asp	Asp	Gly	Asn	Leu	Lys	Ile	Ser	Trp	245	250	255	
Asp	Ser	Gln	Thr	Met	Ala	Pro	Phe	Pro	Leu	Gln	Tyr	Gln	Val	Lys	Tyr	260	265	270	
Leu	Glu	Asn	Ser	Thr	Ile	Val	Arg	Glu	Ala	Ala	Glu	Ile	Val	Ser	Ala	275	280	285	
Thr	Ser	Leu	Leu	Val	Asp	Ser	Val	Leu	Pro	Gly	Ser	Ser	Tyr	Glu	Val	290	295	300	
Gln	Val	Arg	Ser	Lys	Arg	Leu	Asp	Gly	Ser	Gly	Val	Trp	Ser	Asp	Trp	305	310	315	320
Ser	Ser	Pro	Gln	Val	Phe	Thr	Thr	Gln	Asp	Val	Val	Tyr	Phe	Pro	Pro	325	330	335	
Lys	Ile	Leu	Thr	Ser	Val	Gly	Ser	Asn	Ala	Ser	Phe	His	Cys	Ile	Tyr	340	345	350	
Lys	Asn	Glu	Asn	Gln	Ile	Ile	Ser	Ser	Lys	Gln	Ile	Val	Trp	Trp	Arg	355	360	365	
Asn	Leu	Ala	Glu	Lys	Ile	Pro	Glu	Ile	Gln	Tyr	Ser	Ile	Val	Ser	Asp	370	375	380	
Arg	Val	Ser	Lys	Val	Thr	Phe	Ser	Asn	Leu	Lys	Ala	Thr	Arg	Pro	Arg	385	390	395	400
Gly	Lys	Phe	Thr	Tyr	Asp	Ala	Val	Tyr	Cys	Cys	Asn	Glu	Gln	Ala	Cys	405	410	415	
His	His	Arg	Tyr	Ala	Glu	Leu	Tyr	Val	Ile	Asp	Val	Asn	Ile	Asn	Ile	420	425	430	
Ser	Cys	Glu	Thr	Asp	Gly	Tyr	Leu	Thr	Lys	Met	Thr	Cys	Arg	Trp	Ser	435	440	445	
Pro	Ser	Thr	Ile	Gln	Ser	Leu	Val	Gly	Ser	Thr	Val	Gln	Leu	Arg	Tyr	450	455	460	
His	Arg	Arg	Ser	Leu	Tyr	Cys	Pro	Asp	Ser	Pro	Ser	Ile	His	Pro	Thr	465	470	475	480
Ser	Glu	Pro	Lys	Asn	Cys	Val	Leu	Gln	Arg	Asp	Gly	Phe	Tyr	Glu	Cys	485	490	495	
Val	Phe	Gln	Pro	Ile	Phe	Leu	Leu	Ser	Gly	Tyr	Thr	Met	Trp	Ile	Arg	500	505	510	

Ile	Asn	His	Ser	Leu	Gly	Ser	Leu	Asp	Ser	Pro	Pro	Thr	Cys	Val	Leu
		515					520					525			
Pro	Asp	Ser	Val	Val	Lys	Pro	Leu	Pro	Pro	Ser	Asn	Val	Lys	Ala	Glu
	530					535					540				
Ile	Thr	Val	Asn	Thr	Gly	Leu	Leu	Lys	Val	Ser	Trp	Glu	Lys	Pro	Val
545					550					555					560
Phe	Pro	Glu	Asn	Asn	Leu	Gln	Phe	Gln	Ile	Arg	Tyr	Gly	Leu	Ser	Gly
				565					570					575	
Lys	Glu	Ile	Gln	Trp	Lys	Thr	His	Glu	Val	Phe	Asp	Ala	Lys	Ser	Lys
			580					585					590		
Ser	Ala	Ser	Leu	Leu	Val	Ser	Asp	Leu	Cys	Ala	Val	Tyr	Val	Val	Gln
		595					600					605			
Val	Arg	Cys	Arg	Arg	Leu	Asp	Gly	Leu	Gly	Tyr	Trp	Ser	Asn	Trp	Ser
	610					615					620				
Ser	Pro	Ala	Tyr	Thr	Leu	Val	Met	Asp	Val	Lys	Val	Pro	Met	Arg	Gly
625					630					635					640
Pro	Glu	Phe	Trp	Arg	Lys	Met	Asp	Gly	Asp	Val	Thr	Lys	Lys	Glu	Arg
				645					650					655	
Asn	Val	Thr	Leu	Leu	Trp	Lys	Pro	Leu	Thr	Lys	Asn	Asp	Ser	Leu	Cys
			660					665					670		
Ser	Val	Arg	Arg	Tyr	Val	Val	Lys	His	Arg	Thr	Ala	His	Asn	Gly	Thr
		675					680					685			
Trp	Ser	Glu	Asp	Val	Gly	Asn	Arg	Thr	Asn	Leu	Thr	Phe	Leu	Trp	Thr
	690					695					700				
Glu	Pro	Ala	His	Thr	Val	Thr	Val	Leu	Ala	Val	Asn	Ser	Leu	Gly	Ala
705					710					715					720
Ser	Leu	Val	Asn	Phe	Asn	Leu	Thr	Phe	Ser	Trp	Pro	Met	Ser	Lys	Val
				725					730					735	
Ser	Ala	Val	Glu	Ser	Leu	Ser	Ala	Tyr	Pro	Leu	Ser	Ser	Ser	Cys	Val
			740					745					750		
Ile	Leu	Ser	Trp	Thr	Leu	Ser	Pro	Asp	Asp	Tyr	Ser	Leu	Leu	Tyr	Leu
		755					760					765			
Val	Ile	Glu	Trp	Lys	Ile	Leu	Asn	Glu	Asp	Asp	Gly	Met	Lys	Trp	Leu
	770					775					780				
Arg	Ile	Pro	Ser	Asn	Val	Lys	Lys	Phe	Tyr	Ile	His	Asp	Asn	Phe	Ile
785					790					795					800
Pro	Ile	Glu	Lys	Tyr	Gln	Phe	Ser	Leu	Tyr	Pro	Val	Phe	Met	Glu	Gly
				805					810					815	
Val	Gly	Lys	Pro	Lys	Ile	Ile	Asn	Gly	Phe	Thr	Lys	Asp	Ala	Ile	Asp

	820		825		830	
Lys	Gln	Gln	Asn	Asp	Ala	Gly
	835					Leu
						Tyr
						Val
						Ile
						Val
						Pro
						Ile
						Ile
						Ile
Ser	Ser	Cys	Val	Leu	Leu	Leu
	850					Gly
						Thr
						Leu
						Leu
						Ile
						Ser
						His
						Gln
						Arg
Met	Lys	Lys	Leu	Phe	Trp	Asp
	865					Asp
						Val
						Pro
						Asn
						Pro
						Lys
						Asn
						Cys
						Ser
Trp	Ala	Gln	Gly	Leu	Asn	Phe
				885		Gln
						Lys
						Asp
						Ile
						Ser
						Leu
						His
						Glu
						Val
Phe	Ile	Phe	Arg			
			900			

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2468 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
 - CODING REGION: 1-2415
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: A20 (OB-Re)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATGATGTGTC	AGAAATTCTA	TGTGGTTTTG	TTACACTGGG	AATTTCTTTA	TGTGATAGCT	60
GCACTTAACC	TGGCATATCC	AATCTCTCCC	TGGAAATTTA	AGTTGTTTTG	TGGACCACCG	120
AACACAACCG	ATGACTCCTT	TCTCTCACCT	GCTGGAGCCC	CAAACAATGC	CTCGGCTTTG	180
AAGGGGGCTT	CTGAAGCAAT	TGTTGAAGCT	AAATTTAATT	CAAGTGGTAT	CTACGTTCTT	240
GAGTTATCCA	AAACAGTCTT	CCACTGTTGC	TTTGGGAATG	AGCAAGGTCA	AAACTGCTCT	300
GCACTCACAG	ACAACACTGA	AGGGAAGACA	CTGGCTTCAG	TAGTGAAGGC	TTCAGTTTTT	360
CGCCAGCTAG	GTGTAAACTG	GGACATAGAG	TGCTGGATGA	AAGGGGACTT	GACATTATTC	420
ATCTGTCATA	TGGAGCCATT	ACCTAAGAAC	CCCTTCAAGA	ATTATGACTC	TAAGGTCCAT	480
CTTTTATATG	ATCTGCCTGA	AGTCATAGAT	GATTGCCTC	TGCCCCACT	GAAAGACAGC	540
TTTCAGACTG	TCCAATGCAA	CTGCAGTCTT	CGGGGATGTG	AATGTCATGT	GCCGGTACCC	600

AGAGCCAAAC	TCAACTACGC	TCTTCTGATG	TATTTGGAAA	TCACATCTGC	CGGTGTGAGT	660
TTTCAGTCAC	CTCTGATGTC	ACTGCAGCCC	ATGCTTGTTG	TGAAACCCGA	TCCACCCTTA	720
GGTTTGCATA	TGGAAGTCAC	AGATGATGGT	AATTTAAAGA	TTTCTTGGA	CAGCCAAACA	780
ATGGCACCAT	TTCCGCTTCA	ATATCAGGTG	AAATATTTAG	AGAATTCTAC	AATTGTAAGA	840
GAGGCTGCTG	AAATTGTCTC	AGCTACATCT	CTGCTGGTAG	ACAGTGTGCT	TCCTGGATCT	900
TCATATGAGG	TCCAGGTGAG	GAGCAAGAGA	CTGGATGGTT	CAGGAGTCTG	GAGTGACTGG	960
AGTTCACCTC	AAGTCTTTAC	CACACAAGAT	GTTGTGTATT	TTCCACCCAA	AATTCTGACT	1020
AGTGTTGGAT	CGAATGCTTC	TTTTCATTCG	ATCTACAAAA	ACGAAAACCA	GATTATCTCC	1080
TCAAAACAGA	TAGTTTGGTG	GAGGAATCTA	GCTGAGAAAA	TCCCTGAGAT	ACAGTACAGC	1140
ATTGTGAGTG	ACCGAGTTAG	CAAAGTTACC	TTCTCCAACC	TGAAAGCCAC	CAGACCTCGA	1200
GGGAAGTTTA	CCTATGACGC	AGTGTACTGC	TGCAATGAGC	AGGCGTGCCA	TCACCGCTAT	1260
GCTGAATTAT	ACGTGATCGA	TGTCAATATC	AATATATCAT	GTGAAACTGA	CGGGTACTTA	1320
ACTAAAATGA	CTTGCAGATG	GTCACCCAGC	ACAATCCAAT	CACTAGTGGG	AAGCACTGTG	1380
CAGCTGAGGT	ATCACAGGCG	CAGCCTGTAT	TGTCCTGATA	GTCCATCTAT	TCATCCTACG	1440
TCTGAGCCCA	AAAAGTGCCT	CTTACAGAGA	GACGGCTTTT	ATGAATGTGT	TTTCCAGCCA	1500
ATCTTTCTAT	TATCTGGCTA	TACAATGTGG	ATCAGGATCA	ACCATTCTTT	AGGTTCACTT	1560
GACTCGCCAC	CAACGTGTGT	CCTTCCTGAC	TCCGTAGTAA	AACCACTACC	TCCATCTAAC	1620
GTAAAAGCAG	AGATTACTGT	AAACACTGGA	TTATTGAAAG	TATCTTGGA	AAAGCCAGTC	1680
TTTCCGGAGA	ATAACCTTCA	ATTCCAGATT	CGATATGGCT	TAAGTGGA	AGAAATACAA	1740
TGGAAGACAC	ATGAGGTATT	CGATGCAAAG	TCAAAGTCTG	CCAGCCTGCT	GGTGTGAGAC	1800
CTCTGTGCAG	TCTATGTGGT	CCAGGTTTCG	TGCCGGCGGT	TGGATGGACT	AGGATATTGG	1860
AGTAATTGGA	GCAGTCCAGC	CTATACGCTT	GTCATGGATG	TAAAAGTTCC	TATGAGAGGG	1920
CCTGAATTTT	GGAGAAAAAT	GGATGGGGAC	GTTACTAAAA	AGGAGAGAAA	TGTCACCTTG	1980
CTTTGGAAGC	CCCTGACGAA	AAATGACTCA	CTGTGTAGTG	TGAGGAGGTA	CGTGGTGAAG	2040
CATCGTACTG	CCCACAATGG	GACGTGGTCA	GAAGATGTGG	GAAATCGGAC	CAATCTCACT	2100
TTCTGTGGA	CAGAACCAGC	GCACACTGTT	ACAGTTCTGG	CTGTCAATTC	CCTCGGCGCT	2160
TCCCTTGTGA	ATTTTAACTT	TACCTTCTCA	TGGCCCATGA	GTAAAGTGAG	TGCTGTGGAG	2220
TCACTCAGTG	CTTATCCCCCT	GAGCAGCAGC	TGTGTCATCC	TTTCCTGGAC	ACTGTCACCT	2280
GATGATTATA	GTCTGTTATA	TCTGGTTATT	GAATGGAAGA	TCCTTAATGA	AGATGATGGA	2340

ATGAAGTGGC TTAGAATTCC CTCGAATGTT AAAAAGTTTT ATATCCACGG TATGTGTACT 2400
 GTACTTTTCA TGGATTAGTA TGACACTGTA GACTGGCAAT TCTGATAATA AATCATTTAA 2460
 TGACAACC 2468

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 805 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: OB-Re

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met	Met	Cys	Gln	Lys	Phe	Tyr	Val	Val	Leu	Leu	His	Trp	Glu	Phe	Leu	1	5	10	15
Tyr	Val	Ile	Ala	Ala	Leu	Asn	Leu	Ala	Tyr	Pro	Ile	Ser	Pro	Trp	Lys	20	25	30	
Phe	Lys	Leu	Phe	Cys	Gly	Pro	Pro	Asn	Thr	Thr	Asp	Asp	Ser	Phe	Leu	35	40	45	
Ser	Pro	Ala	Gly	Ala	Pro	Asn	Asn	Ala	Ser	Ala	Leu	Lys	Gly	Ala	Ser	50	55	60	
Glu	Ala	Ile	Val	Glu	Ala	Lys	Phe	Asn	Ser	Ser	Gly	Ile	Tyr	Val	Pro	65	70	75	80
Glu	Leu	Ser	Lys	Thr	Val	Phe	His	Cys	Cys	Phe	Gly	Asn	Glu	Gln	Gly	85	90	95	
Gln	Asn	Cys	Ser	Ala	Leu	Thr	Asp	Asn	Thr	Glu	Gly	Lys	Thr	Leu	Ala	100	105	110	
Ser	Val	Val	Lys	Ala	Ser	Val	Phe	Arg	Gln	Leu	Gly	Val	Asn	Trp	Asp	115	120	125	
Ile	Glu	Cys	Trp	Met	Lys	Gly	Asp	Leu	Thr	Leu	Phe	Ile	Cys	His	Met	130	135	140	
Glu	Pro	Leu	Pro	Lys	Asn	Pro	Phe	Lys	Asn	Tyr	Asp	Ser	Lys	Val	His				

145	150	155	160
Leu Leu Tyr Asp 165	Leu Pro Glu Val Ile 170	Asp Asp Ser Pro 175	Leu Pro Pro 175
Leu Lys Asp Ser 180	Phe Gln Thr Val 185	Gln Cys Asn Cys Ser 190	Leu Arg Gly 190
Cys Glu Cys His 195	Val Pro Val 200	Pro Arg Ala Lys 205	Leu Asn Tyr Ala Leu 205
Leu Met Tyr Leu 210	Glu Ile Thr Ser 215	Ala Gly Val Ser 220	Phe Gln Ser Pro 220
Leu Met Ser Leu 225	Gln Pro Met Leu 230	Val Val Lys Pro 235	Asp Pro Pro Leu 240
Gly Leu His Met 245	Glu Val Thr Asp 250	Asp Gly Asn Leu 255	Lys Ile Ser Trp 255
Asp Ser Gln Thr 260	Met Ala Pro Phe 265	Pro Leu Gln Tyr 270	Gln Val Lys Tyr 270
Leu Glu Asn Ser 275	Thr Ile Val Arg 280	Glu Ala Ala Glu 285	Ile Val Ser Ala 285
Thr Ser Leu Leu 290	Val Asp Ser Val 295	Leu Pro Gly Ser 300	Ser Tyr Glu Val 300
Gln Val Arg Ser 305	Lys Arg Leu Asp 310	Gly Ser Gly Val 315	Trp Ser Asp Trp 320
Ser Ser Pro Gln 325	Val Phe Thr Thr 330	Gln Asp Val Val 335	Tyr Phe Pro Pro 335
Lys Ile Leu Thr 340	Ser Val Gly Ser 345	Asn Ala Ser Phe 350	His Cys Ile Tyr 350
Lys Asn Glu Asn 355	Gln Ile Ile Ser 360	Ser Lys Gln Ile 365	Val Trp Trp Arg 365
Asn Leu Ala Glu 370	Lys Ile Pro Glu 375	Ile Gln Tyr Ser 380	Ile Val Ser Asp 380
Arg Val Ser Lys 385	Val Thr Phe Ser 390	Asn Leu Lys Ala 395	Thr Arg Pro Arg 400
Gly Lys Phe Thr 405	Tyr Asp Ala Val 410	Tyr Cys Cys Asn 415	Glu Gln Ala Cys 415
His His Arg Tyr 420	Ala Glu Leu Tyr 425	Val Ile Asp Val 430	Asn Ile Asn Ile 430
Ser Cys Glu Thr 435	Asp Gly Tyr Leu 440	Thr Lys Met Thr 445	Cys Arg Trp Ser 445

Pro 450	Ser	Thr	Ile	Gln	Ser	Leu 455	Val	Gly	Ser	Thr	Val 460	Gln	Leu	Arg	Tyr
His 465	Arg	Arg	Ser	Leu	Tyr 470	Cys	Pro	Asp	Ser	Pro 475	Ser	Ile	His	Pro	Thr 480
Ser	Glu	Pro	Lys	Asn 485	Cys	Val	Leu	Gln	Arg 490	Asp	Gly	Phe	Tyr	Glu 495	Cys
Val	Phe	Gln	Pro 500	Ile	Phe	Leu	Leu	Ser 505	Gly	Tyr	Thr	Met	Trp 510	Ile	Arg
Ile	Asn	His 515	Ser	Leu	Gly	Ser	Leu 520	Asp	Ser	Pro	Pro	Thr 525	Cys	Val	Leu
Pro	Asp 530	Ser	Val	Val	Lys	Pro 535	Leu	Pro	Pro	Ser	Asn 540	Val	Lys	Ala	Glu
Ile 545	Thr	Val	Asn	Thr	Gly 550	Leu	Leu	Lys	Val	Ser 555	Trp	Glu	Lys	Pro	Val 560
Phe	Pro	Glu	Asn	Asn 565	Leu	Gln	Phe	Gln	Ile 570	Arg	Tyr	Gly	Leu	Ser 575	Gly
Lys	Glu	Ile	Gln 580	Trp	Lys	Thr	His	Glu 585	Val	Phe	Asp	Ala	Lys 590	Ser	Lys
Ser	Ala	Ser 595	Leu	Leu	Val	Ser	Asp 600	Leu	Cys	Ala	Val	Tyr 605	Val	Val	Gln
Val	Arg 610	Cys	Arg	Arg	Leu	Asp 615	Gly	Leu	Gly	Tyr	Trp 620	Ser	Asn	Trp	Ser
Ser 625	Pro	Ala	Tyr	Thr	Leu 630	Val	Met	Asp	Val	Lys 635	Val	Pro	Met	Arg	Gly 640
Pro	Glu	Phe	Trp	Arg 645	Lys	Met	Asp	Gly	Asp 650	Val	Thr	Lys	Lys	Glu 655	Arg
Asn	Val	Thr	Leu 660	Leu	Trp	Lys	Pro	Leu 665	Thr	Lys	Asn	Asp	Ser 670	Leu	Cys
Ser	Val	Arg 675	Arg	Tyr	Val	Val	Lys 680	His	Arg	Thr	Ala	His 685	Asn	Gly	Thr
Trp	Ser 690	Glu	Asp	Val	Gly	Asn 695	Arg	Thr	Asn	Leu	Thr 700	Phe	Leu	Trp	Thr
Glu 705	Pro	Ala	His	Thr	Val 710	Thr	Val	Leu	Ala	Val 715	Asn	Ser	Leu	Gly	Ala 720
Ser	Leu	Val	Asn	Phe 725	Asn	Leu	Thr	Phe	Ser 730	Trp	Pro	Met	Ser	Lys 735	Val
Ser	Ala	Val	Glu 740	Ser	Leu	Ser	Ala	Tyr 745	Pro	Leu	Ser	Ser	Ser 750	Cys	Val
Ile	Leu	Ser	Trp	Thr	Leu	Ser	Pro	Asp	Asp	Tyr	Ser	Leu	Leu	Tyr	Leu

755	760	765
Val Ile Glu Trp Lys Ile Leu Asn Glu Asp Asp Gly Met Lys Trp Leu		
770	775	780
Arg Ile Pro Ser Asn Val Lys Lys Phe Tyr Ile His Gly Met Cys Thr		
785	790	795 800
Val Leu Phe Met Asp		
805		

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: C-terminal
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: OB-Ra
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Asn Phe Gln Lys Arg Thr Asp Leu
1 5

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 276 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: C-terminal
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: OB-Rb

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Asn	Phe	Gln	Lys	Pro	Glu	Thr	Phe	Glu	Gln	Leu	Phe	Thr	Lys	His	Ala	
1				5					10					15		
Glu	Ser	Val	Ile	Phe	Gly	Pro	Leu	Leu	Leu	Glu	Pro	Glu	Pro	Ile	Ser	
			20					25					30			
Glu	Glu	Ile	Ser	Val	Asp	Thr	Ala	Trp	Lys	Asn	Lys	Asp	Glu	Met	Val	
		35					40					45				
Pro	Ala	Ala	Met	Val	Ser	Leu	Leu	Trp	Thr	Thr	Pro	Asp	Pro	Glu	Ser	
	50					55					60					
Ser	Ser	Ile	Cys	Ile	Ser	Asp	Gln	Cys	Asn	Ser	Ala	Asn	Phe	Ser	Gly	
65					70				75						80	
Ser	Gln	Ser	Thr	Gln	Val	Cys	Glu	Asp	Glu	Cys	Gln	Arg	Gln	Pro	Ser	
				85					90					95		
Val	Lys	Tyr	Ala	Thr	Leu	Val	Ser	Asn	Asp	Lys	Leu	Val	Glu	Thr	Asp	
			100					105					110			
Glu	Glu	Gln	Gly	Phe	Ile	His	Ser	Pro	Val	Ser	Asn	Cys	Ile	Ser	Ser	
		115					120					125				
Asn	His	Ser	Pro	Leu	Arg	Gln	Ser	Phe	Ser	Ser	Ser	Ser	Trp	Glu	Thr	
	130					135					140					
Glu	Ala	Gln	Thr	Phe	Phe	Leu	Leu	Ser	Asp	Gln	Gln	Pro	Thr	Met	Ile	
145					150					155					160	
Ser	Pro	Gln	Leu	Ser	Phe	Ser	Gly	Leu	Asp	Glu	Leu	Leu	Glu	Leu	Glu	
				165					170					175		
Gly	Ser	Phe	Pro	Glu	Glu	Asn	His	Arg	Glu	Lys	Ser	Val	Cys	Tyr	Leu	
			180					185					190			
Gly	Val	Thr	Ser	Val	Asn	Arg	Arg	Glu	Ser	Gly	Val	Leu	Leu	Thr	Gly	
		195					200					205				
Glu	Ala	Gly	Ile	Leu	Cys	Thr	Phe	Pro	Ala	Gln	Cys	Leu	Phe	Ser	Asp	
	210					215					220					
Ile	Arg	Ile	Leu	Gln	Glu	Arg	Cys	Ser	His	Phe	Val	Glu	Asn	Asn	Leu	
225					230					235					240	
Ser	Leu	Gly	Thr	Ser	Gly	Glu	Asn	Phe	Gly	Pro	Tyr	Met	Pro	Gln	Phe	
				245					250					255		
Gln	Thr	Cys	Ser	Thr	His	Ser	His	Lys	Ile	Met	Glu	Asn	Lys	Met	Cys	
			260					265					270			
Asp	Phe	Thr	Val													
			275													

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: C-terminal
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: OB-Rc

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Asn	Phe	Gln	Lys	Val	Thr	Val
1				5		

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: C-terminal
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: OB-Rd

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Asn	Phe	Gln	Lys	Asp	Ile	Ser	His	Glu	Val	Phe	Ile	Phe	Arg
1				5					10				

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: not relevant

- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: C-terminal
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: OB-Re

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Phe	Tyr	Ile	His	Gly	Met	Cys	Thr	Val	Leu	Phe	Met	Asp
1				5					10			

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: internal
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: OB-Ra/db/db

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Pro	Gln	Lys	Arg	Thr	Asp	Thr	Leu
1				5			

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vii) IMMEDIATE SOURCE:

(B) CLONE: OB-Rb/wt

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Pro Gln Lys Pro Glu Thr
1 5

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GATGGAGGGA AA

12

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GATGGAGGTA AA

12

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATCTTGGGTT CTCTGAAGAA

20

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GAGATTGTCA GTCACAGCCT C

21

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ATCTGAATTG GAATCAAATA CAC

23

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

AAATCTGTTA TCCTTCTGAA AC

22

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ACACTGTAA TTTCACACCA GAG

23

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AGTCATTCAA ACCATTAGTT TAGG

24

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TGGATAAACC CTTGCTCTTC A

21

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TGAACACAAC AACATAAAGC CC

22

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AGGCTCCCTC AGGGCCAC

18

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GTGACTGAAT GAAGATGTAA TATAC

25

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TGTTATATCT GGTTATTGAA TGG

23

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CATTAAATGA TTTATTATCA GAATTGC

27

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Glu	Pro	Leu	Pro	Lys	Asn	Pro	Phe	Lys	Asn	Tyr	Asp	Ser	Lys
1				5					10				

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

His	Arg	Arg	Ser	Leu	Tyr	Cys	Pro	Asp	Ser	Pro	Ser	Ile	His	Pro	Thr
1				5					10					15	
Ser Glu Pro Lys															
20															

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Gln	Arg	Met	Lys	Lys	Leu	Phe	Trp	Asp	Asp	Val	Pro	Asn	Pro	Lys	Asn
1				5					10					15	
Cys Ser Trp															

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 166 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: 7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

AGGGNAAGCG CCGAGGGAAT TGACAGCCAG AACTGTAACA GTGTGCGCTG GTTCTGTCCA	60
CAGGAAAGTG AGATTGGTCC GATTTCCCAC ATCTTCTGAC CACGTCCCAT TGTGGGCAGT	120
ACGATGCTTC ACCACGTACC TCCTCACACT ACACAGTGAG TCATTT	166

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 320 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
 (B) CLONE: 11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GGTGAAGCAT CGTACTGCCC ACAATGGGAC GTGGTCAGAA GATGTGGGAA ATCGGACCAA	60
TCTCACTTTC CTGTGGACAG AACCAGCGCA CACTGTTACA GTTCTGGCTG TCAATTCCCT	120
CGGCGCTTCC CTTGTGAATT TTAACCTTAC CTTCTCATGG CCCATGAGTA AAGTGAGTGC	180
TGTGGAGTCA CTCAGTGCTT ATCCCCTGAG CAGCAGCTGT GTCATCCTTT CCTGGACACT	240
GTCACCTGAT GATTATAGTC TGTTATATCT GGTTATTGAA TGGAAGATCC TTAATGAAGA	300
TGATGGAATG AAGTGGCTTA	320

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 158 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: 42

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GATTACTGGA GATGCAGTTG CTGACAGGAC TATGGATAAA CCCTTGCTCT TCATCAGTTT	60
CCACTAGTTT ATCGTTGCTG ACCAGAGTTG CATATTTAAC TGAGGGTTGT CTCTGACACT	120
CATCCTCACA GGTTACCTGG GTGCTCTGAG ACCCAGAG	158

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: 46

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

AGAGAGATCC CTGACCCTAG TTAGATCTGT TTTCAGGCTC TGTGTTTCATT TGATGTTTCAG	60
AAGTCAGCAA GGTTCTCATA TGTCTGAGT TAGTAAGATG TCTCAGGGTT CCCCCATCAG	120
CTAACAACCA CTTTGACATG AGAAGGCAGA AAGTTAAAGA ACACTACTTG GTGTTTTACT	180
TAAAGATACG AG	192

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 168 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: 58

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

AGACTGACAA GGAAGTTTT TCATCTAACA AGCAAGCAAA GGAAGTCTT ATGTNCTGTG	60
ANGAACCAAG GNAGCTCAGA TGTCACCATA GTCATCATGA ACTCGAGTGA CTCTGCCACT	120
GTTCCCCCAG GATGTGCTTG GANGATAATC CTGCGCAAGA AACAGATA	168

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 259 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: S3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

AGAATTATGA CTCTAAGGTC CATCTTTTAT ATGATCTGCC TGAAGTCATA GATGATTCGC	60
CTCTGCCCCC ACTGAAAGAC AGNTTTCAGA CTGTCCAATG NAACTGCAGT CTTCGGGGAT	120
GTGAATGTCA TGTGCCAGTA CCCAGAGCCA AACTCAACTA CGCTCTTCTG ATGTATTTGG	180
NAATCACATC TGCCGGTGTG AGTTTTTCAGT CACCTCTGAT GTCAGTGCAG CCCATGCTTG	240
TTGTGAAACC CGATCCACC	259

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 250 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: S14

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CTTCAACAAT TGGTTCAGAA GCCCCCTTCA AAGCCGAGGC ATTGTTTGGG GCTCCAGCAG	60
GTGAGAGAAA GGAGTCATCG GTTGTGTTCG GTGGTCCACA AAACAACCTTA AATTTCCAGG	120
GAGAGATTGG ATATGCCAGG TTAAGTGCAG CTATCACATA AAGAAATTCC CAGTGTAACA	180
AAACCACATA GANTTTCTAA CACATCATCT TTCTTCAGAG GTGTACACCT GGATTTGCAG	240
AACGATTCCCT	250

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CCGAGGGAAT TGACAGCC	18
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(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CTCACTGTGT AGTGTGAGGA GG

22

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

TCCTGTGGAC AGAACCAGC

19

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TGACACAGCT GCTGCTCAG

19

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GGTCTCAGAG CACCCAGGTA

20

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

AGAGAGATCC CTGACCCTAG TT

22

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

AACTTTCTGC CTCCTTCTC ATGTCA

26

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

TTTCTCATCT AACAGCAAG CA

22

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

ATCTGTTTCT TGCGCAGGAT

20

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CATTGTTTGG GGCTCCAG

18

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

AATCGTTCTG CAAATCCAGG

20

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

TGAAGTCATA GATGATTCGC C

21

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GTTCGTACCC GACGTCCTG

20